**Supplementary materials**

**for**

Claudinéia Pereira Costa, Clycie Aparecida da Silva Machado, and Tiago Mauricio Francoy. 2021. Assessment of genetic diversity and population structure of *Eulaema nigrita* (Hymenoptera: Apidae: Euglossini) as a factor of habitat type in Brazilian Atlantic forest fragments. The Canadian Entomologist

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**Table S1.** Linear distances between sites (km). PEMD: Parque Estadual Morro do Diabo; PETAR: Parque Estadual Turístico do Alto Ribeira; PINDA: Pindamonhangaba; UBA: Ubatuba.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | PEMD | PETAR | PINDA | UBA |
| PEMD |  |  |  |  |
| PETAR | 426.844 |  |  |  |
| PINDA | 690.377 | 362.454 |  |  |
| UBA | 735.006 | 376.405 | 69.110 |  |

**Table S2.** Information about sampling sites and *Eulaema nigrita*. \*Relative abundance = *El. nigrita* abundance compared to the total species abundance presented at that location. +N of collected individuals = number of specimens for *El. nigrita* in each area; in parentheses: number total of specimens from all collected species in each sampling site. Parque Estadual Morro do Diabo; PETAR: Parque Estadual Turístico do Alto Ribeira; PINDA: Pindamonhangaba; UBA: Ubatuba. SSR: simple sequence repeat

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **PINDA** | **UBA** | **PEMD** | **PETAR** |
| **Habitat** | Semi-deciduous | Rainforest | Semi-deciduous | Rainforest |
| **Relative abundance (%) \*** | 21.68 | 3.14 | 7.8 | 75 |
| **N of collected individuals +** | 31 (143) | 19 (606) | 55 (705) | 21 (28) |
| **N of individuals used for SSR** | 30 | 17 | 49 | 20 |
| **N of individuals used for mtDNA** | 30 | 18 | 41 | 16 |

**Table S3.** Pairwise *Phi*PT values (below diagonal) among populations of *Eulaema nigrita*. PEMD: Parque Estadual Morro do Diabo; PETAR: Parque Estadual Turístico do Alto Ribeira. PINDA: Pindamonhangaba; UBA: Ubatuba. (α = 0.05).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | PEMD | PETAR | PINDA | UBA |
| PEMD |  |  |  |  |
| PETAR | 0.000 |  |  |  |
| PINDA | 0.087 | 0.102 |  |  |
| UBA | 0.099 | 0.095 | 0.057 |  |

**Table S4.** Summary of the analysis of molecular variance results for males of *Eulaema nigrita*. *d.f.:* degree of freedom; SS: sum of squared observations; MS: mean of squared observations; *Phi*RT: proportion of the total genetic variance that is due to the variance between regions; *Phi*PR: proportion of the total genetic variance that is due to the variance among populations within a region; *Phi*PT: proportion of the total genetic variance that is due to the variance among individuals within a variant.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Source** | ***d.f.*** | **SS** | **MS** | **Estimated Variance** | **Percentage (%)** | ***Phi* Statistic** | **Value** | ***P-*value** |
| **Among Regions** | 1 | 5.278 | 5.278 | 0.011 | 1 | PhiRT | 0.006 | 0.222 |
| **Among Populations within Regions** | 2 | 9.794 | 4.897 | 0.108 | 5 | PhiPR | 0.054 | 0.001 |
| **Within Populations** | 112 | 210.989 | 1.884 | 1.884 | 94 | PhiPT | 0.06 | 0.001 |
| **Total** | 115 | 226.06 |  | 2.004 | 100 |  |  |  |

**Table S5.** Percentage of males of *Eulaema nigrita* correctly (self-pop) or incorrectly (other pop) attributed to their original population by the assignment test. PEMD: Parque Estadual Morro do Diabo; PETAR: Parque Estadual Turístico do Alto Ribeira. PINDA: Pindamonhangaba; UBA: Ubatuba.

|  |  |  |
| --- | --- | --- |
| **Population** | **Self-Pop** | **Other Pop** |
| **PEMD** | 24 | 25 |
| **PETAR** | 13 | 7 |
| **PINDA** | 16 | 14 |
| **UBA** | 8 | 9 |
| **Total** | 61 | 55 |
| **Percent** | 53% | 47% |

***R code***

#package

library("lme4")

library("MuMIn")

library("multcomp")

library("diveRsity")

library("lmtest")

#calculate Allelic richness, upload file from Genalex, format Genepop2D

genepop2D <- read.csv("teste.csv", sep = ";", header = F)

basicMicro\_results <- divBasic(infile = genepop2D, outfile = 'out', gp = 2)

AR <- basicMicro\_results[["Allelic\_richness"]]

#LMMs code

variables.AR <- read.csv("inputmodel.csv")

#model null

modelNULL<-lmer(AllelicRichness ~ 1 + (1 | Locus), variables.AR, REML = FALSE)

#model 1: Habitat and Relative Abundance as fixed factors

modelMANAG <- lmer(AllelicRichness ~ Habitat + AbundanceRelative + (1 | Locus), variables.AR, REML = FALSE)

summary(modelMANAG)

plot(modelMANAG)

anova(modelMANAG, modelNULL)

r.squaredGLMM(modelMANAG)

posthoc <- glht(modelMANAG, linfct = mcp(Habitat = "Tukey"))

summary(posthoc)

lrtest(modelMANAG, modelNULL)

#model 2: Habitat alone as fixed factor

modelMANAG2 <- lmer(AllelicRichness ~ Habitat + (1 | Locus), variables.AR, REML = FALSE)

summary(modelMANAG2)

plot(modelMANAG2)

anova(modelMANAG2, modelNULL)

r.squaredGLMM(modelMANAG2)

posthoc2 <- glht(modelMANAG2, linfct = mcp(Habitat = "Tukey"))

summary(posthoc2)

lrtest(modelMANAG2, modelNULL)

#model 3: Relative abundance alone as fixed factor

modelMANAG3<- lmer(AllelicRichness ~ AbundanceRelative + (1 | Locus), variables.AR, REML = FALSE)

summary(modelMANAG3)

plot(modelMANAG3)

anova(modelMANAG3, modelNULL)

r.squaredGLMM(modelMANAG3)

variables.AR$AbundanceRelative = as.factor(variables.AR$AbundanceRelative)

posthoc3 <- glht(modelMANAG3, linfct = mcp(AbundanceRelative = "Tukey"))

summary(posthoc3)

lrtest(modelMANAG3, modelNULL)

#model 4: Interaction between relative abundance and habitat as fixed factor

modelMANAG4 <- lmer(AllelicRichness ~ Habitat:AbundanceRelative + (1 | Locus), variables.AR, REML = FALSE)

summary(modelMANAG4)

plot(modelMANAG4)

anova(modelMANAG4, modelNULL)

r.squaredGLMM(modelMANAG4)

posthoc4 <- glht(modelMANAG4, linfct = mcp(Habitat = "Tukey"))

summary(posthoc4)

lrtest(modelMANAG4, modelNULL)